

## **RAW SEQUENCE LISTING**

**The Biotechnology Systems Branch of the Scientific and Technical  
Information Center (STIC) no errors detected.**

Application Serial Number: 10/541, 270A  
Source: PCT  
Date Processed by STIC: 03/06/2006

# ***ENTERED***



PCT

## RAW SEQUENCE LISTING

DATE: 03/06/2006

PATENT APPLICATION: US/10/541,270A

TIME: 15:16:17

Input Set : A:\ITR0043YP SEQLIST.TXT

Output Set : N:\CRF4\03062006\J541270A.raw

4 <110> APPLICANT: Monaci, Paolo  
 5 Nuzzo, Maurizio  
 6 La Monica, Nicola  
 7 Ciliberto, Gennaro  
 8 Lahm, Armin  
 10 <120> TITLE OF INVENTION: RHESUS HER2/NEU, NUCLEOTIDES ENCODING  
 11 SAME AND USES THEREOF  
 13 <130> FILE REFERENCE: ITR0043YP  
 C--> 15 <140> CURRENT APPLICATION NUMBER: US/10/541,270A  
 C--> 16 <141> CURRENT FILING DATE: 2005-07-01  
 18 <150> PRIOR APPLICATION NUMBER: PCT/EP03/14997  
 19 <151> PRIOR FILING DATE: 2003-12-29  
 21 <150> PRIOR APPLICATION NUMBER: 60/437,846  
 22 <151> PRIOR FILING DATE: 2003-01-03  
 24 <160> NUMBER OF SEQ ID NOS: 43  
 26 <170> SOFTWARE: FastSEQ for Windows Version 4.0  
 28 <210> SEQ ID NO: 1  
 29 <211> LENGTH: 3768  
 30 <212> TYPE: DNA  
 31 <213> ORGANISM: Rhesus Monkey  
 33 <400> SEQUENCE: 1  
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 35 gcgggcaccc aagtgtgcac cggcacagac atgaagctgc ggctccctgc cagtcccag 120  
 36 acccacctgg acatgctccg ccacctctac cagggctgcc aggtggtgca gggtaacctg 180  
 37 gaactcacct acctgcccac caatgccagc ctctccttcc tgcaggatat ccaggaggtg 240  
 38 cagggctacg tgctcatcgc tcacaaccaa gtgaggcagg tcccactgca gaggtcgcg 300  
 39 attgtgcgag gcaccagct ctttgaggac aactatgcc tggccgtgct agacaatgga 360  
 40 gacctgctga acaataccac ccctgtcaca ggggcctccc caggaggcct gcgggagctg 420  
 41 cagcttcgaa gcctcacaga gatcttgaaa ggaggggtct tgatccagcg gaacccccag 480  
 42 ctctgctacc aggacacgat tttgtggaag gacatcttcc ataagaacaa ccagctggct 540  
 43 ctcacactga tcgacaccaa ccgctctcgg gcctgccacc cctgttctcc agtgtgtgtaag 600  
 44 ggctcccgcg gctggggaga gagttctgag gattgtcaga gcctgacgcg cactgtctgt 660  
 45 gccggtggct gtgcccgcgt caagggggcca ctgcccactg actgctgcca tgagcagtgt 720  
 46 gctgccggct gcacgggccc caagcactct gactgcctgg cctgcctcca cttcaaccac 780  
 47 agcggcatct gtgarctgca ctgcccagcc ctgggtcacct acaacacaga cacctttgag 840  
 48 tccatgcccc accccgaggg ccggtataca ttcggcgcca gctgtgtgac tgccctgtccc 900  
 49 tacaactacc tttctacgga cgtgggatcc tgcaccctcg tctgccccct gcacaaccaa 960  
 50 gaggtgacag cggaggacgg aacacagcga tgtgagaagt gcagcaagcc ctgtgcccga 1020  
 51 gtgtgctatg gtctgggcat ggagcacttg cgagaggtga gggcggtcac cagtgccaat 1080  
 52 atccaggagt ttgctggctg caagaagatc tttgggagct tggcatttct gccagagagc 1140  
 53 tttgatggcg acccagcctc caacaccgcc ccgcttcagc cggagcagct ccgagtgttt 1200  
 54 gagactctgg aagagatcac aggttaccta tacatctcag catggccaga cagcctgcct 1260  
 55 gaccttagcg tcctccagaa cctgcaagta atccggggac gaattctgca caatggcgcc 1320

CP9-67

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58 ccctgggacc agctcttccg gaacccgcac caagccctgc tccacactgc caaccggcca 1500
59 gaggacgagt gtgtgggcca gggcctggcc tgccaccagc tgtgcgcccg agggcactgc 1560
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61 gtggaggaat gccgagtact gcaggggctc cccaggaggt atgtgaatgc cagacactgt 1680
62 ttgccgtgcc accctgagtg tcagccccag aatggctcag tgacatgttt tggaccggag 1740
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66 ggctgccccg ccgagcagag agccagccct ctgacgtcca tcatctctgc tgtggtgggc 1980
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93 gtcaaagacg tttttgcctt tgggggtgct gtggagaacc ccgagtactt ggcaccccg 3600
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95 tattactggg accaggaccc atcagagcgg ggggctccac ctagcacctt caaagggaca 3720
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98 &lt;210&gt; SEQ ID NO: 2

99 &lt;211&gt; LENGTH: 1255

100 &lt;212&gt; TYPE: PRT

101 &lt;213&gt; ORGANISM: Rhesus Monkey

103 &lt;400&gt; SEQUENCE: 2

104 Met Glu Leu Ala Ala Trp Tyr Arg Trp Gly Leu Leu Leu Ala Leu Leu

105 1 5 10 15

106 Pro Pro Gly Ala Ala Gly Thr Gln Val Cys Thr Gly Thr Asp Met Lys

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107		20		25		30	
108	Leu Arg Leu Pro Ala Ser Pro Glu Thr His Leu Asp Met Leu Arg His						
109		35		40		45	
110	Leu Tyr Gln Gly Cys Gln Val Val Gln Gly Asn Leu Glu Leu Thr Tyr						
111		50		55		60	
112	Leu Pro Thr Asn Ala Ser Leu Ser Phe Leu Gln Asp Ile Gln Glu Val						
113	65		70		75		80
114	Gln Gly Tyr Val Leu Ile Ala His Asn Gln Val Arg Gln Val Pro Leu						
115		85		90		95	
116	Gln Arg Leu Arg Ile Val Arg Gly Thr Gln Leu Phe Glu Asp Asn Tyr						
117		100		105		110	
118	Ala Leu Ala Val Leu Asp Asn Gly Asp Leu Leu Asn Asn Thr Thr Pro						
119		115		120		125	
120	Val Thr Gly Ala Ser Pro Gly Gly Leu Arg Glu Leu Gln Leu Arg Ser						
121		130		135		140	
122	Leu Thr Glu Ile Leu Lys Gly Gly Val Leu Ile Gln Arg Asn Pro Gln						
123	145		150		155		160
124	Leu Cys Tyr Gln Asp Thr Ile Leu Trp Lys Asp Ile Phe His Lys Asn						
125		165		170		175	
126	Asn Gln Leu Ala Leu Thr Leu Ile Asp Thr Asn Arg Ser Arg Ala Cys						
127		180		185		190	
128	His Pro Cys Ser Pro Val Cys Lys Gly Ser Arg Cys Trp Gly Glu Ser						
129		195		200		205	
130	Ser Glu Asp Cys Gln Ser Leu Thr Arg Thr Val Cys Ala Gly Gly Cys						
131		210		215		220	
132	Ala Arg Cys Lys Gly Pro Leu Pro Thr Asp Cys Cys His Glu Gln Cys						
133	225		230		235		240
134	Ala Ala Gly Cys Thr Gly Pro Lys His Ser Asp Cys Leu Ala Cys Leu						
135		245		250		255	
136	His Phe Asn His Ser Gly Ile Cys Glu Leu His Cys Pro Ala Leu Val						
137		260		265		270	
138	Thr Tyr Asn Thr Asp Thr Phe Glu Ser Met Pro Asn Pro Glu Gly Arg						
139		275		280		285	
140	Tyr Thr Phe Gly Ala Ser Cys Val Thr Ala Cys Pro Tyr Asn Tyr Leu						
141		290		295		300	
142	Ser Thr Asp Val Gly Ser Cys Thr Leu Val Cys Pro Leu His Asn Gln						
143	305		310		315		320
144	Glu Val Thr Ala Glu Asp Gly Thr Gln Arg Cys Glu Lys Cys Ser Lys						
145		325		330		335	
146	Pro Cys Ala Arg Val Cys Tyr Gly Leu Gly Met Glu His Leu Arg Glu						
147		340		345		350	
148	Val Arg Ala Val Thr Ser Ala Asn Ile Gln Glu Phe Ala Gly Cys Lys						
149		355		360		365	
150	Lys Ile Phe Gly Ser Leu Ala Phe Leu Pro Glu Ser Phe Asp Gly Asp						
151		370		375		380	
152	Pro Ala Ser Asn Thr Ala Pro Leu Gln Pro Glu Gln Leu Arg Val Phe						
153	385		390		395		400
154	Glu Thr Leu Glu Glu Ile Thr Gly Tyr Leu Tyr Ile Ser Ala Trp Pro						
155		405		410		415	

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156 Asp Ser Leu Pro Asp Leu Ser Val Leu Gln Asn Leu Gln Val Ile Arg
157          420          425          430
158 Gly Arg Ile Leu His Asn Gly Ala Tyr Ser Leu Thr Leu Gln Gly Leu
159          435          440          445
160 Gly Ile Ser Trp Leu Gly Leu Arg Ser Leu Arg Glu Leu Gly Ser Gly
161          450          455          460
162 Leu Ala Leu Ile His His Asn Thr Arg Leu Cys Phe Val His Thr Val
163 465          470          475          480
164 Pro Trp Asp Gln Leu Phe Arg Asn Pro His Gln Ala Leu Leu His Thr
165          485          490          495
166 Ala Asn Arg Pro Glu Asp Glu Cys Val Gly Glu Gly Leu Ala Cys His
167          500          505          510
168 Gln Leu Cys Ala Arg Gly His Cys Trp Gly Pro Gly Pro Thr Gln Cys
169          515          520          525
170 Val Asn Cys Ser Gln Phe Leu Arg Gly Gln Glu Cys Val Glu Glu Cys
171          530          535          540
172 Arg Val Leu Gln Gly Leu Pro Arg Glu Tyr Val Asn Ala Arg His Cys
173 545          550          555          560
174 Leu Pro Cys His Pro Glu Cys Gln Pro Gln Asn Gly Ser Val Thr Cys
175          565          570          575
176 Phe Gly Pro Glu Ala Asp Gln Cys Val Ala Cys Ala His Tyr Lys Asp
177          580          585          590
178 Pro Pro Phe Cys Val Ala Arg Cys Pro Ser Gly Val Lys Pro Asp Leu
179          595          600          605
180 Ser Tyr Met Pro Ile Trp Lys Phe Pro Asp Glu Glu Gly Thr Cys Gln
181          610          615          620
182 Ser Cys Pro Ile Asn Cys Thr His Ser Cys Val Asp Leu Asp Asp Lys
183 625          630          635          640
184 Gly Cys Pro Ala Glu Gln Arg Ala Ser Pro Leu Thr Ser Ile Ile Ser
185          645          650          655
186 Ala Val Val Gly Ile Leu Leu Val Val Val Leu Gly Val Val Phe Gly
187          660          665          670
188 Ile Leu Ile Lys Arg Arg Gln Gln Lys Ile Arg Lys Tyr Thr Met Arg
189          675          680          685
190 Arg Leu Leu Gln Glu Thr Glu Leu Val Glu Pro Leu Thr Pro Ser Gly
191          690          695          700
192 Ala Met Pro Asn Gln Ala Gln Met Arg Ile Leu Lys Glu Thr Glu Leu
193 705          710          715          720
194 Arg Lys Val Lys Val Leu Gly Ser Gly Ala Phe Gly Thr Val Tyr Lys
195          725          730          735
196 Gly Ile Trp Ile Pro Asp Gly Glu Asn Val Lys Ile Pro Val Ala Ile
197          740          745          750
198 Lys Val Leu Arg Glu Asn Thr Ser Pro Lys Ala Asn Lys Glu Ile Leu
199          755          760          765
200 Asp Glu Ala Tyr Val Met Ala Gly Val Gly Ser Pro Tyr Val Ser Arg
201          770          775          780
202 Leu Leu Gly Ile Cys Leu Thr Ser Thr Val Gln Leu Val Thr Gln Leu
203 785          790          795          800
204 Met Pro Tyr Gly Cys Leu Leu Asp His Val Arg Glu Asn Arg Gly Arg

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205				805				810				815		
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207				820				825				830		
208	Met	Ser	Tyr	Leu	Glu	Asp	Val	Arg	Leu	Val	His	Arg	Asp	Leu
209			835					840				845		
210	Arg	Asn	Val	Leu	Val	Lys	Ser	Pro	Asn	His	Val	Lys	Ile	Thr
211		850					855				860			
212	Gly	Leu	Ala	Arg	Leu	Leu	Asp	Ile	Asp	Glu	Thr	Glu	Tyr	His
213	865					870				875				880
214	Gly	Gly	Lys	Val	Pro	Ile	Lys	Trp	Met	Ala	Leu	Glu	Ser	Ile
215				885				890				895		
216	Arg	Arg	Phe	Thr	His	Gln	Ser	Asp	Val	Trp	Ser	Tyr	Gly	Val
217			900					905				910		
218	Trp	Glu	Leu	Met	Thr	Phe	Gly	Ala	Lys	Pro	Tyr	Asp	Gly	Ile
219		915					920				925			
220	Arg	Glu	Ile	Pro	Asp	Leu	Leu	Glu	Lys	Gly	Glu	Arg	Leu	Pro
221		930				935					940			
222	Pro	Ile	Cys	Thr	Ile	Asp	Val	Tyr	Met	Ile	Met	Val	Lys	Cys
223	945				950					955				960
224	Ile	Asp	Ser	Glu	Cys	Arg	Pro	Arg	Phe	Arg	Glu	Leu	Val	Ser
225				965				970				975		
226	Ser	Arg	Met	Ala	Arg	Asp	Pro	Gln	Arg	Phe	Val	Val	Ile	Gln
227			980					985				990		
228	Asp	Leu	Gly	Pro	Ala	Ser	Pro	Leu	Asp	Ser	Thr	Phe	Tyr	Arg
229		995					1000				1005			
230	Leu	Glu	Asp	Asp	Asp	Met	Gly	Asp	Leu	Val	Asp	Ala	Glu	Glu
231		1010				1015				1020				
232	Val	Pro	Gln	Gln	Gly	Phe	Phe	Cys	Pro	Asp	Pro	Ala	Pro	Gly
233	1025				1030					1035				1040
234	Gly	Met	Val	His	His	Arg	His	Arg	Ser	Ser	Ser	Thr	Arg	Ser
235			1045					1050				1055		
236	Gly	Asp	Leu	Thr	Leu	Gly	Leu	Glu	Pro	Ser	Glu	Glu	Glu	Ala
237			1060					1065				1070		
238	Ser	Pro	Arg	Ala	Pro	Ser	Glu	Gly	Thr	Gly	Ser	Asp	Val	Phe
239		1075				1080					1085			
240	Asp	Leu	Gly	Met	Gly	Ala	Ala	Lys	Gly	Leu	Gln	Ser	Leu	Pro
241		1090				1095				1100				
242	Asp	Pro	Ser	Pro	Leu	Gln	Arg	Tyr	Ser	Glu	Asp	Pro	Thr	Val
243	1105				1110					1115				1120
244	Pro	Ser	Glu	Thr	Asp	Gly	Tyr	Val	Ala	Pro	Leu	Thr	Cys	Ser
245			1125					1130				1135		
246	Pro	Glu	Tyr	Val	Asn	Gln	Pro	Asp	Val	Arg	Pro	Gln	Pro	Pro
247			1140					1145				1150		
248	Gln	Glu	Gly	Pro	Leu	Ser	Pro	Ala	Arg	Pro	Thr	Gly	Ala	Thr
249		1155				1160				1165				
250	Arg	Pro	Lys	Thr	Leu	Ser	Pro	Gly	Lys	Asn	Gly	Val	Val	Lys
251		1170				1175				1180				
252	Phe	Ala	Phe	Gly	Gly	Ala	Val	Glu	Asn	Pro	Glu	Tyr	Leu	Ala
253	1185				1190					1195				1200

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:41; Xaa Pos. 517,647,1075

**VERIFICATION SUMMARY**

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L:15 M:270 C: Current Application Number differs, Replaced Current Application Number

L:16 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:816 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:41 after pos.:512

M:341 Repeated in SeqNo=41